

<212> DNA

<213> Homo sapiens

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agctcaagac cacctcgata agagaatgtg cacatcctta cattaagcct gaaagaacca 240
ttagtttaag gagggtgaga taagagaccc ttttcctacc agcaaccaga cttactacta 300
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<210> 2

<211> 66

<212> PRT

<213> Homo sapiens

<400> 2

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Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
20 25 30
His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
35 40 45
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
50 55 60
Pro Arg
65

<210> 3

<211> 690

<212> DNA

<213> Homo sapiens

<400> 3

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tcatggcaag aagatcttga gaatatgtat ctggacaccc ctcggtatcg aggcaggtca 240
taccatgacc ggaagtcaaa agttgacctg gataggctca atgatgatgc caagcgttac 300
agttgcactc ccaggaatta ctcggtcaat ataagagaag agctgaagtt ggccaatgtg 360
gtcttctttc cacgttgacct cctcgtgcag cgctgtggag gaaattgtgg ctgtggaact 420
gtcaaactgg agtcctgcac atgcaattca gggaaaaccg tgaaaaagta tcatgaggta 480
ttacagtttg agcctggcca catcaagagg aggggtagag ctaagaccat ggctctagtt 540
gacatccagt tggatcacca tgaacgatgc gattgtatct gcagctcaag accacctcga 600
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gataagagac ccttttccta ccagcaaccc 690

<210> 4

<211> 200

<212> PRT

<213> Homo sapiens

<400> 4

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1 5 10 15
Thr Ser Ser Val Ser Gly Tyr Pro Tyr Asn Ser Pro Ser Val Thr Asp
20 25 30
Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp
35 40 45
Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu

50

55

60

Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser
65 70 75 80

Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp
85 90 95

Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg
100 105 110

Glu Glu Leu Lys Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu
115 120 125

Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val Lys Leu Glu
130 135 140

Ser Cys Thr Cys Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val
145 150 155 160

Leu Gln Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr
165 170 175

Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys
180 185 190

Ile Cys Ser Ser Arg Pro Pro Arg
195 200

<210> 5

<211> 1934

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(966)

<223>

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1 5 10 15																
cag agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca	96															
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr																
20 25 30																
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Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp																
35 40 45																
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50 55 60																
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Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly																
65 70 75 80																
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Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr																
85 90 95																
aac caa att aaa atc aca ttc aag tcc gat gac tac ttt gtg gct aaa	336															
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys																
100 105 110																
cct gga ttc aag att tat tat tct ttg ctg gaa gat ttc caa ccc gca	384															
Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala																
115 120 125																
gca gct tca gag acc aac tgg gaa tct gtc aca agc tct att tca ggg	432															
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly																
130 135 140																
gta tcc tat aac tct cca tca gta acg gat ccc act ctg att gcg gat	480															
Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp																
145 150 155 160																
gct ctg gac aaa aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc	528															
Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu																
165 170 175																
aag tac ttc aat cca gag tca tgg caa gaa gat ctt gag aat atg tat	576															
Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr																
180 185 190																
ctg gac acc cct cgg tat cga ggc agg tca tac cat gac cgg aag tca	624															
Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser																
195 200 205																
aaa gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac agt tgc	672															
Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys																

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<210> 6

<211> 322

<212> PRT

<213> Homo sapiens

<400> 6

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20 25 30

Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
35 40 45

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
50 55 60

Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
65 70 75 80

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
85 90 95

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
100 105 110

Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
115 120 125

Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
130 135 140

Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
145 150 155 160

204050"62998084

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Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala	
165 170 175	
gct tca gag acc aac tgg gaa tct gtc aca agc tct att tca ggg gta	754
Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val	
180 185 190	
tcc tat aac tct cca tca gta acg gat ccc act ctg att gcg gat gct	802
Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala	
195 200 205	
ctg gac aaa aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag	850
Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys	
210 215 220 225	
tac ttc aat cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg	898
Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu	
230 235 240	
gac acc cct cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa	946
Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys	
245 250 255	
gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac agt tgc act	994
Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr	
260 265 270	
ccc agg aat tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat	1042
Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn	
275 280 285	
gtg gtc ttc ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat	1090
Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn	
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tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg	1138
Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly	
310 315 320	
aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag cct ggc cac	1186
Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His	
325 330 335	
atc aag agg agg ggt aga gct aag acc atg gct cta gtt gac atc cag	1234
Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln	
340 345 350	
ttg gat cac cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct	1282
Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro	
355 360 365	
cga taa gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg	1338
Arg	
370	
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<210> 8

<211> 370

<212> PRT

<213> Homo sapiens

<400> 8

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Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
1           5           10          15

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Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
20           25           30

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Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
35           40           45

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Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val

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50

55

60

Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
65 70 75 80

Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
85 90 95

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
100 105 110

Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
115 120 125

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
130 135 140

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145 150 155 160

Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
165 170 175

Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
180 185 190

Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
195 200 205

Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
210 215 220

Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
225 230 235 240

Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
245 250 255

Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
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Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
275 280 285

<213> Homo sapiens

<220>

<221> misc_feature

<223> PDGF/VEGF-homology domain of PDGF-D

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Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu
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Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly
20 25 30

Gly Asn Cys Gly Cys Gly Thr Val Lys Leu Glu Ser Cys Thr Cys Asn
35 40 45

Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro
50 55 60

Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp
65 70 75 80

Ile Gln Leu Asp His His Glu Arg Cys Asp Cys
85 90

<210> 11

<211> 88

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> PDGF/VEGF-homology domain of PDGF-C

<400> 11

204060" E299900T

Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys Arg
1 5 10 15

Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly
20 25 30

Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val
35 40 45

Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro
50 55 60

Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu
65 70 75 80

Glu His His Glu Glu Cys Asp Cys
85

<210> 12

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> PDGF/VEGF-homology domain of PDGF-A

<400> 12

Cys Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp
1 5 10 15

Pro Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys
20 25 30

Arg Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser
35 40 45

Arg Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg
50 55 60

Lys Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu
65 70 75 80

Glu Cys Ala Cys

<210> 13

<211> 84

<212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

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<221> misc feature
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<223> PDGF/VEGF-homology domain of PDGF-B

<400> 13

Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
1 5 10 15

Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
20 25 30

Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
35 40 45

Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
50 55 60

Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
65 70 75 80

Ala Cys Lys Cys

204060 "E399000"

<210> 14
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> PDGF/VEGF-homology domain of VEGF-165

<400> 14
Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp
1 5 10 15
Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys
20 25 30
Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu
35 40 45
Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly Gln
50 55 60
His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu Cys
65 70 75

<210> 15
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> PDGF/VEGF-homology domain of PlGF-2

204060" E299900T

<400> 15

Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu Tyr Pro Ser
1 5 10 15

Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu Leu Arg Cys
20 25 30

Thr Gly Cys Cys Gly Asp Glu Asp Leu His Cys Val Pro Val Glu Thr
35 40 45

Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly Asp Arg Pro
50 55 60

Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys Glu Cys
65 70 75

<210> 16

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> PDGF/VEGF-homology domain of VEGF-B167

<400> 16

Cys Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly
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Thr Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys
20 25 30

Gly Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln
35 40 45

His Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln

60

Leu Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys
65 70 75

<213> Homo sapiens

<223> PDGF/VEGF-homology domain of VEGF-C

Cys

<212> PRT

204060" E299000

<213> Homo sapiens

<220>

<221> misc_feature

<223> PDGF/VEGF-homology domain of VEGF-D

<400> 18

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Thr Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys
20 25 30

Gly Gly Cys Cys Asn Glu Glu Gly Val Met Cys Met Asn Thr Ser Thr
35 40 45

Ser Tyr Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser
50 55 60

Val Pro Glu Leu Val Pro Val Lys Ile Ala Asn His Thr Gly Cys Lys
65 70 75 80

Cys

<210> 19

<211> 118

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> CUB domain of PDGF-D

<400> 19

204020 "E23500"

Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg
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Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His
20 25 30

Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly
35 40 45

Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val
50 55 60

Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly
65 70 75 80

His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys
85 90 95

Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys
100 105 110

Ile Tyr Tyr Ser Leu Leu
115

<210> 20

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> CUB domain 1 of BMP-1

<400> 20

Cys Gly Glu Thr Leu Gln Asp Ser Thr Gly Asn Phe Ser Ser Pro Glu
1 5 10 15

204060" E269200T

Tyr Pro Asn Gly Tyr Ser Ala His Met His Cys Val Trp Arg Ile Ser
20 25 30

Val Thr Pro Gly Glu Lys Ile Ile Leu Asn Phe Thr Ser Leu Asp Leu
35 40 45

Tyr Arg Ser Arg Leu Cys Trp Tyr Asp Tyr Val Glu Val Arg Asp Gly
50 55 60

Phe Trp Arg Lys Ala Pro Leu Arg Gly Arg Phe Cys Gly Ser Lys Leu
65 70 75 80

Pro Glu Pro Ile Val Ser Thr Asp Ser Arg Leu Trp Val Glu Phe Arg
85 90 95

Ser Ser Ser Asn Trp Val Gly Lys Gly Phe Phe Ala Val Tyr Glu Ala
100 105 110

Ile

<210> 21

<211> 112

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> CUB domain 2 of BMP-1

<400> 21

Cys Gly Gly Asp Val Lys Lys Asp Tyr Gly His Ile Gln Ser Pro Asn
1 5 10 15

Tyr Pro Asp Asp Tyr Arg Pro Ser Lys Val Cys Ile Trp Arg Ile Gln
20 25 30

Val Ser Glu Gly Phe His Val Gly Leu Thr Phe Gln Ser Phe Glu Ile

35

40

45

Glu Arg Met Asp Ser Cys Ala Tyr Asp Tyr Leu Glu Val Arg Asp Gly
50 55 60

His Ser Glu Ser Ser Thr Leu Ile Gly Arg Tyr Cys Gly Tyr Glu Lys
65 70 75 80

Pro Asp Asp Ile Lys Ser Thr Ser Ser Arg Leu Trp Leu Lys Phe Val
85 90 95

Ser Asp Gly Ser Ile Asn Lys Ala Gly Phe Ala Val Asn Phe Phe Lys
100 105 110

<210> 22

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> CUB domain 3 of BMP-1

<400> 22

Cys Gly Gly Phe Leu Thr Lys Leu Asn Gly Ser Ile Thr Ser Pro Gly
1 5 10 15

Trp Pro Lys Glu Tyr Pro Pro Asn Lys Asn Cys Ile Trp Gln Leu Val
20 25 30

Ala Pro Thr Gln Tyr Arg Ile Ser Leu Gln Phe Asp Phe Phe Glu Thr
35 40 45

Glu Gly Asn Asp Val Cys Lys Tyr Asp Phe Val Glu Val Arg Ser Gly
50 55 60

Leu Thr Ala Asp Ser Lys Leu His Gly Lys Phe Cys Gly Ser Glu Lys
65 70 75 80

Pro Glu Val Ile Thr Ser Gln Tyr Asn Asn Met Arg Val Glu Pro Lys
85 90 95

Ser Asp Asn Thr Val Ser Lys Lys Gly Phe Lys Ala His Phe Phe Ser
100 105 110

Glu

<210> 23

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> CUB domain 1 of Neuropilin

<400> 23

Gly Asp Thr Ile Lys Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly
1 5 10 15

Tyr Pro His Ser Tyr His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln
20 25 30

Ala Pro Asp Pro Tyr Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe
35 40 45

Asp Leu Glu Asp Arg Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp
50 55 60

Gly Glu Asn Glu Asn Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile
65 70 75 80

Ala Pro Pro Pro Val Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe
85 90 95

Val Ser Asp Tyr Glu Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu
100 105 110

Ile

<210> 24

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> CUB domain 2 of Neuropilin

<400> 24

Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser Pro Gly
1 5 10 15

Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile Val Phe
20 25 30

Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe Asp Leu
35 40 45

Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr Asp Arg
50 55 60

Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile Gly Arg
65 70 75 80

Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser Gly Ile
85 90 95

Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu Gly Phe
100 105 110

Ser Ala Asn Tyr Ser Val Leu
115

<210> 25

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> can be any amino acid residue

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> can be any amino acid residue

<400> 25

Pro	Xaa	Cys	Leu	Leu	Val	Xaa	Arg	Cys	Gly	Gly	Asn	Cys	Gly	Cys
1				5					10				15	

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward PCR primer used to amplify a 327 bp DNA fragment from a human fetal lung cDNA library

<400> 26

gtcgtggaac tgtcaactgg

<210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reverse PCR primer used to amplify a 327 bp DNA fragment from a human fetal lung cDNA library

<400> 27
 ctcagcaacc acttggtggtc 20

<210> 28
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Adaptor primer 1 (Clontech) used to amplify the sequence found at the 5' end of PDGF-D

<400> 28
 ccataccta acgactcact atagggc 27

<210> 29
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Adaptor primer 2 (Clontech) used to amplify the sequence found at the 5' end of PDGF-D

<400> 29
 agtgggatcc gttactgatg gagagttat 29

<400> 32

Met Ser Leu Phe Gly Leu Leu Leu Val Thr Ser Ala Leu Ala Gly Gln
1 5 10 15

Arg Arg Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
20 25 30

Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
35 40 45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
50 55 60

His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
65 70 75 80

Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
85 90 95

Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
100 105 110

Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
115 120 125

Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
130 135 140

Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145 150 155 160

Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
165 170 175

Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
180 185 190

Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
195 200 205

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Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
210 215 220

Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
225 230 235 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
245 250 255

Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
260 265 270

Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
275 280 285

His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
290 295 300

Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
305 310 315 320

His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
325 330 335

Cys Val Cys Arg Gly Ser Thr Gly Gly
340 345

- <210> 33
- <211> 26
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence: Forward PCR primer for the cD
NA encoding amino acid residues 24-370 of SEQ ID NO:8 (PDGF-D)
- <220>
- <221> misc_feature
- <223> Primer includes a XbaI site for in frame cloning

26

<211> 46

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Reverse PCR primer for amplification of the cDNA encoding amino acid residues 24-370 of SEQ ID NO:8 (PDGF-D)

 $\langle 220 \rangle$

<221> misc feature

<223> Primer includes an EcoRI site and sequences encoding for a C-terminal 6X His tag preceded by an enterokinase site

46

<210> 35

<211> 1252

<212> DNA

<213> Murinae gen. sp.

<400>	35							
atgcaacggc	tcgtttttagt	ctccattctc	ctgtgcgcgga	acttttagctg	ctatccggac		60	
actttttgcga	ctccgcagag	agcatccatc	aaagctttgc	gcaatgccaa	cctcaggaga		120	
gatgagagca	atcacctcac	agacttgtac	cagagagagg	agaacattca	ggtgacaagc		180	
aatggccatg	tgcagagtcc	tcgcttcccg	aacagctacc	caaggaacct	gcttctgaca		240	
tggtggctcc	gttcccagga	gaaaacacgg	atacaactgt	cotttgacca	tcaattcgga		300	
ctagaggaag	cagaaaatga	catttgtagg	tatgactttg	tggaaagttga	agaagtctca		360	

gagagcagca ctgttgtcag aggaagatgg tgtggccaca aggagatccc tccaaggata 420
acgtcaagaa caaaccagat taaaatcaca tttaagtctg atgactactt tgtggcaaaa 480
cctggattca agatttatta ttcatttgtg gaagatttcc aaccggaagc agcctcagag 540
accaactggg aatcagtcac aagctctttc tctgggggtg cctatcactc tocatcaata 600
acggacccca ctctcactgc tgatgccctg gacaaaactg tcgcagaatt cgataccgtg 660
gaagatctac ttaagcactt caatccagtg tcttggaag atgatctgga gaatttgtat 720
ctggacaccc ctcatatag aggcaggtca taccatgatc ggaagtccaa agtggacctg 780
gacaggctca atgatgatgt caagcgttac agttgcactc ccaggaatca ctctgtgaac 840
ctcagggagg agctgaagct gaccaatgca gtcttcttcc cacgatgcct cctcgtgcag 900
cgctgtggtg gcaactgtgg ttgcggaact gtcaactgga agtcctgcac atgcagctca 960
gggaagacag tgaagaagta tcatgaggta ttgaagtttg agcctggaca tttcaagaga 1020
aggggcaaag ctaagaatat ggctcttggt gatatccagc tggatcatca tgagcgtgt 1080
gactgtatct gcagctcaag accacctcga taaaacacta tgcacatctg tactttgatt 1140
atgaaaggac ctttaggtta caaaaaccct aagaagcttc taatctcagt gcaatgaatg 1200
catatggaaa tgttgctttg ttagtgccat ggcaagaaga agcaaataatc at 1252

<210> 36

<211> 370

<212> PRT

<213> Murinae gen. sp.

<400> 36

Met Gln Arg Leu Val Leu Val Ser Ile Leu Leu Cys Ala Asn Phe Ser
1 5 10 15

Cys Tyr Pro Asp Thr Phe Ala Thr Pro Gln Arg Ala Ser Ile Lys Ala
20 25 30

Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
35 40 45

Leu Tyr Gln Arg Glu Glu Asn Ile Gln Val Thr Ser Asn Gly His Val

50		55		60	
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr	65	70	75	80	
Trp Trp Leu Arg Ser Gln Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp	85	90	95		
His Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp	100	105	110		
Phe Val Glu Val Glu Glu Val Ser Glu Ser Ser Thr Val Val Arg Gly	115	120	125		
Arg Trp Cys Gly His Lys Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr	130	135	140		
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys	145	150	155	160	
Pro Gly Phe Lys Ile Tyr Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu	165	170	175		
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Phe Ser Gly	180	185	190		
Val Ser Tyr His Ser Pro Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp	195	200	205		
Ala Leu Asp Lys Thr Val Ala Glu Phe Asp Thr Val Glu Asp Leu Leu	210	215	220		
Lys His Phe Asn Pro Val Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr	225	230	235	240	
Leu Asp Thr Pro His Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser	245	250	255		
Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Val Lys Arg Tyr Ser Cys	260	265	270		
Thr Pro Arg Asn His Ser Val Asn Leu Arg Glu Glu Leu Lys Leu Thr	275	280	285		

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Asn Ala Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
290 295 300

Asn Cys Gly Cys Gly Thr Val Asn Trp Lys Ser Cys Thr Cys Ser Ser
305 310 315 320

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Lys Phe Glu Pro Gly
325 330 335

His Phe Lys Arg Arg Gly Lys Ala Lys Asn Met Ala Leu Val Asp Ile
340 345 350

Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
355 360 365

Pro Arg
370

- <210> 37
- <211> 1234
- <212> DNA
- <213> Murinae gen. sp.

<400> 37
atgcaacggc tcgttttagt ctccattctc ctgtgcgcga actttagctg ctatccggac 60
acttttgcca ctccgcagag agcatccatc aaagctttgc gcaatgccaa cctcaggaga 120
gatgacttgt accagagaga ggagaacatt caggtgacaa gcaatggcca tgtgcagagt 180
cctcgcttcc cgaacagcta cccaaggaac ctgcttctga catgggtggct ccgttcccag 240
gagaaaacac ggatacaact gtcctttgac catcaattcg gactagagga agcagaaaat 300
gacatttgta ggtatgactt tgtggaagtt gaagaagtct cagagagcag cactgttgtc 360
agaggaagat ggtgtggcca caaggagatc cctccaagga taacgtcaag aacaaaccag 420
attaaaaatca catttaagtc tgatgactac tttgtggcaa aacctggatt caagatttat 480
tattcatttg tggaagattt ccaaccggaa gcagcctcag agaccaactg ggaatcagtc 540
acaagctott tctctggggt gtctatcac tctccatcaa taacggaccc cactctcact 600

gctgatgccc tggacaaaac tgtcgcagaa ttcgataccg tggagatct acttaagcac 660
 ttcaatccag tgtcttggca agatgatctg gagaatttgt atctggacac ccctcattat 720
 agaggcaggt cataccatga tcggaagtcc aaagtggacc tggacaggct caatgatgat 780
 gtcaagcggt acagttgcac tcccaggaat cactctgtga acctcagga ggagctgaag 840
 ctgaccaatg cagtcttctt cccacgatgc ctctctgtgc agcgtgtgg tggcaactgt 900
 ggttgcgga ctgtcaactg gaagtcctgc acatgcagct caggaagac agtgaagaag 960
 tatcatgagg tattgaagtt tgagcctgga catttcaaga gaaggggcaa agctaagaat 1020
 atggctcttg ttgatatcca gctggatcat catgagcgat gtgactgtat ctgcagctca 1080
 agaccaoctc gataaaacac tatgcacatc tgtacttga ttatgaaagg acctttaggt 1140
 tacaaaaacc ctaagaagct tctaattctca gtgcaatgaa tgcatatgga aatgttgctt 1200
 tgttagtgcc atggcaagaa gaagcaaata tcat 1234

<210> 38

<211> 364

<212> PRT

<213> Murinae gen. sp.

<400> 38

Met Gln Arg Leu Val Leu Val Ser Ile Leu Leu Cys Ala Asn Phe Ser
 1 5 10 15

Cys Tyr Pro Asp Thr Phe Ala Thr Pro Gln Arg Ala Ser Ile Lys Ala
 20 25 30

Leu Arg Asn Ala Asn Leu Arg Arg Asp Asp Leu Tyr Gln Arg Glu Glu
 35 40 45

Asn Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro
 50 55 60

Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln
 65 70 75 80

Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu
 85 90 95

Tyr His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly
 325 330 335

Lys Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu
 340 345 350

Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg
 355 360

<210> 39

<211> 768

<212> DNA

<213> Murinae gen. sp.

<400> 39

atgcaacggc tcgttttagt ctccattctc ctgtgcgcga acttttagctg ctatccggac	60
actttttgcga ctccgcagag agcatccatc aaagctttgc gcaatgccaa cctcaggaga	120
gatgacttgt accagagaga ggagaacatt caggtgacaa gcaatggcca tgtgcagagt	180
cctcgcttcc cgaacagcta cccaaggaac ctgcttctga catggtggct ccgttcccag	240
gagaaaaacac ggatacaact gtcctttgac catcaattcg gactagagga agcagaaaaat	300
gacatttgta ggtatgactt tgtggaagtt gaagaagtct cagagagcag cactgttgtc	360
agaggaagat ggtgtggcca caaggagatc cctccaagga taacgtcaag aacaaaccag	420
attaaaatca catttaagtc tgatgactac tttgtggcaa aacctggatt caagatttat	480
tattcatttg tggaagattt ccaaccggaa gcagcctcag agaccaactg ggaatcagtc	540
acaagctctt tctctggggt gtccatcac tctccatcaa taacggaccc cactctcact	600
gctgatgccc tggacaaaaac tgtcgcagaa ttcgataccg tggaagatct acttaagcac	660
ttcaatccag tgtcttggca agatgatctg gagaatttgt atctggacac ccctcattat	720
agaggcaggt cataccatga tcggaagtcc aaaggatttg aagtttga	768

<210> 40

<211> 255

<212> PRT

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<213> Murinae gen. sp.

<400> 40

Met Gln Arg Leu Val Leu Val Ser Ile Leu Leu Cys Ala Asn Phe Ser
1 5 10 15

Cys Tyr Pro Asp Thr Phe Ala Thr Pro Gln Arg Ala Ser Ile Lys Ala
20 25 30

Leu Arg Asn Ala Asn Leu Arg Arg Asp Asp Leu Tyr Gln Arg Glu Glu
35 40 45

Asn Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro
50 55 60

Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln
65 70 75 80

Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu
85 90 95

Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Glu
100 105 110

Val Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys
115 120 125

Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr
130 135 140

Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr
145 150 155 160

Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn
165 170 175

Trp Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro
180 185 190

Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val
195 200 205

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2040E0E2A5A00F

Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val
210 215 220

Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr
225 230 235 240

Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Gly Ile Glu Val
245 250 255

<210> 41

<211> 19

<212> DNA

<213> Murinae gen. sp.

<400> 41
caaatgcaac ggctcgttt

19

<210> 42

<211> 24

<212> DNA

<213> Murinae gen. sp.

<400> 42
gatatttgct tcttcttgcc atgg

24